

Appendix I: BLAST search of GenBank Accession No. W26469 against the human genomic plus transcript (G+T) database  
 BLASTN 2.2.20+  
 Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 301E3H6C01S

Database: Human build 36.3 RNA, reference, and HuRef assemblies

49,942 sequences; 5,818,011,736 total letters

Query= g[1307375]gb[W26469.1] 32f4 Human retina cDNA randomly primed  
 sublibrary Homo sapiens cDNA, mRNA sequence.  
 Length=754

Sequences producing significant alignments:	Score (Bits)	E Value
ref NT_007933.14 Hs7_8090 Homo sapiens chromosome 7 genomic c...	426	1e-116
ref NW_001839071.2 Hs7_WGA464_36 Homo sapiens chromosome 7 ge...	426	1e-116
ref NT_024524.13 Hs13_24680 Homo sapiens chromosome 13 genom...	44.6	0.16
ref NT_019546.15 Hs12_19702 Homo sapiens chromosome 12 genom...	44.6	0.16
ref NW_001838061.2 Hs12_WGA770_36 Homo sapiens chromosome 12 ...	44.6	0.16
ref NW_001838074.1 Hs13_WGA783_36 Homo sapiens chromosome 13 ...	44.6	0.16
ref NT_033927.7 Hs11_34082 Homo sapiens chromosome 11 genomic...	41.0	2.0
ref NT_008705.15 Hs10_8862 Homo sapiens chromosome 10 genomic...	41.0	2.0
ref NT_009714.16 Hs12_9871 Homo sapiens chromosome 12 genomic...	41.0	2.0
ref NT_008413.17 Hs9_8570 Homo sapiens chromosome 9 genomic c...	41.0	2.0
ref NW_001839149.2 Hs9_WGA542_36 Homo sapiens chromosome 9 ge...	41.0	2.0
ref NW_001837932.2 Hs10_WGA641_36 Homo sapiens chromosome 10 ...	41.0	2.0
ref NW_001838052.1 Hs12_WGA761_36 Homo sapiens chromosome 12 ...	41.0	2.0
ref NW_001838028.2 Hs11_WGA737_36 Homo sapiens chromosome 11 ...	41.0	2.0
ref XM_001715194.1  PREDICTED: Homo sapiens WD repeat domain ...	39.2	6.8
ref XM_293354.9  PREDICTED: Homo sapiens WD repeat domain 42C...	39.2	6.8
ref XM_942624.3  PREDICTED: Homo sapiens WD repeat domain 42C...	39.2	6.8
ref NT_025741.14 Hs6_25897 Homo sapiens chromosome 6 genomic ...	39.2	6.8
ref NT_022517.17 Hs3_22673 Homo sapiens chromosome 3 genomic ...	39.2	6.8
ref NT_026437.11 Hs14_26604 Homo sapiens chromosome 14 genom...	39.2	6.8
ref NT_006576.15 Hs5_6733 Homo sapiens chromosome 5 genomic c...	39.2	6.8
ref NT_016354.18 Hs4_16510 Homo sapiens chromosome 4 genomic ...	39.2	6.8
ref NT_011757.15 HsX_11914 Homo sapiens chromosome X genomic ...	39.2	6.8
ref NT_022135.15 Hs2_22291 Homo sapiens chromosome 2 genomic ...	39.2	6.8
ref NT_005334.15 Hs2_5491 Homo sapiens chromosome 2 genomic c...	39.2	6.8
ref NT_022184.14 Hs2_22340 Homo sapiens chromosome 2 genomic ...	39.2	6.8
ref NT_010194.16 Hs15_10351 Homo sapiens chromosome 15 genom...	39.2	6.8
ref NT_023133.12 Hs5_23289 Homo sapiens chromosome 5 genomic ...	39.2	6.8
ref NW_001838218.2 Hs15_WGA927_36 Homo sapiens chromosome 15 ...	39.2	6.8
ref NW_001838848.1 Hs2_WGA241_36 Homo sapiens chromosome 2 ge...	39.2	6.8
ref NW_001838768.1 Hs2_WGA161_36 Homo sapiens chromosome 2 ge...	39.2	6.8
ref NW_001838766.1 Hs2_WGA159_36 Homo sapiens chromosome 2 ge...	39.2	6.8
ref NW_001838920.1 Hs4_WGA313_36 Homo sapiens chromosome 4 ge...	39.2	6.8
ref NW_001838929.1 Hs5_WGA322_36 Homo sapiens chromosome 5 ge...	39.2	6.8
ref NW_001838111.1 Hs14_WGA820_36 Homo sapiens chromosome 14 ...	39.2	6.8
ref NW_001842360.1 HsX_WGA1321_36 Homo sapiens chromosome X g...	39.2	6.8
ref NW_001838954.2 Hs5_WGA347_36 Homo sapiens chromosome 5 ge...	39.2	6.8
ref NW_001838877.2 Hs3_WGA270_36 Homo sapiens chromosome 3 ge...	39.2	6.8



```

          ||||| || | || |||||
Sbjct  2602400 GCACAACAAAGAGGCAAGGG 2602380

```

>ref|NT\_024524.13|Hs13\_24680 Homo sapiens chromosome 13 genomic contig, reference as  
Length=67740325

Features flanking this part of subject sequence:

7592 bp at 5' side: hypothetical protein

16093 bp at 3' side: fibronectin type III domain containing 3A isoform 1

Score = 44.6 bits (48), Expect = 0.16

Identities = 32/36 (88%), Gaps = 1/36 (2%)

Strand=Plus/Plus

```

Query  140      TAAAGCAGCCCAAGAAAAACAGACCAACAGAAAAG 175
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  30544201 TAAAGCAGCCCAAGAAAAACAGAACAA-AGATAAG 30544235

```

>ref|NT\_019546.15|Hs12\_19702 Homo sapiens chromosome 12 genomic contig, reference as  
Length=32815934

Features flanking this part of subject sequence:

2785 bp at 5' side: D-amino-acid oxidase

9168 bp at 3' side: SV2 related protein

Score = 44.6 bits (48), Expect = 0.16

Identities = 40/48 (83%), Gaps = 2/48 (4%)

Strand=Plus/Plus

```

Query  152      AAGAAA-AACAGACCAACAGAAAAGCAATGAGAGAAAGGAT-GAAGGT 197
          ||||| || ||| || ||||| || ||||| ||||| ||||| |||||
Sbjct  32779285 AAGAAAGAAAAGAAAGAAAAGAAAAGAGAGAAAGGATGGAAGGT 32779332

```

>ref|NW\_001838061.2|Hs12\_WGA770\_36 Homo sapiens chromosome 12 genomic contig, altern  
(based on HuRef SCAF\_1103279188362)  
Length=32873191

Features flanking this part of subject sequence:

8830 bp at 5' side: SV2 related protein

2949 bp at 3' side: D-amino-acid oxidase

Score = 44.6 bits (48), Expect = 0.16

Identities = 40/48 (83%), Gaps = 2/48 (4%)

Strand=Plus/Minus

```

Query  152      AAGAAA-AACAGACCAACAGAAAAGCAATGAGAGAAAGGAT-GAAGGT 197
          ||||| || ||| || ||||| || ||||| ||||| ||||| |||||
Sbjct  77998 AAGAAAGAAAAGAAAGAAAAGAAAAGAGAGAAAGGATGGAAGGT 77951

```

>ref|NW\_001838074.1|Hs13\_WGA783\_36 Homo sapiens chromosome 13 genomic contig, altern  
(based on HuRef SCAF\_1103279188353)  
Length=6801713

Features flanking this part of subject sequence:

7591 bp at 5' side: hypothetical protein

16117 bp at 3' side: fibronectin type III domain containing 3A isoform 1

Score = 44.6 bits (48), Expect = 0.16  
Identities = 32/36 (88%), Gaps = 1/36 (2%)  
Strand=Plus/Plus

Query	140	TAAAAGCAGCCCAAGAAAAACAGACCAACAGAAAAAG	175
Spict	3561241	TAAAAGCAGCCAAAGAAAAACAGAACAA-AGATAAG	3561275

>ref|NT\_033927.7|Hs11\_34082 Homo sapiens chromosome 11 genomic contig, reference assembly  
Length=17911127

Features in this part of subject sequence:  
transmembrane protein 135

Score = 41.0 bits (44), Expect = 2.0  
Identities = 27/29 (93%), Gaps = 1/29 (3%)  
Strand=Plus/Minus

```
Query    141      AAAAGCAGCCCAAGAAAAACAGACCAACA   169
          |||||
Sbjct    17085496 AAAAGCAGCCCAAGAAAAA-AGACCCACA   17085499
```

```
>ref|NT_008705.15|Hs10_8862 Homo sapiens chromosome 10 genomic contig, reference assembly
Length=20794160
```

Features flanking this part of subject sequence:  
24944 bp at 5' side: cyclin Y isoform 2  
11430 bp at 3' side: connexin40.1

Score = 41.0 bits (44), Expect = 2.0  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Plus

```

Query 154      GAAAAACAGACCAACAGAAAAGCAA 178
               |||||
Sbjct 17858367 GAAAAACAGAACCAACAGAAAAGCAA 17858391

```

```
>ref|NT_009714.16|Hs12_9871 Homo sapiens chromosome 12 genomic contig, reference assembly
Length=27615668
```

Features flanking this part of subject sequence:  
149869 bp at 5' side: intermediate filament tail domain containing 1  
352356 bp at 3' side: Ras association (RalGDS/AF-6) domain family 8

Score = 41.0 bits (44), Expect = 2.0  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Plus

```

Query    140      TAAAAGCAGCCCAAGAAAAACAGAC    164
          |||||
Sbjct    18614871 TAAAAGCAGCCCAAGAAAAACAGAC    18614895

```

>ref|NT\_008413.17|Hs9\_8570 Homo sapiens chromosome 9 genomic contig, reference assembly  
Length=39653686

Features flanking this part of subject sequence:

14584 bp at 5' side: FRAS1 related extracellular matrix 1  
288432 bp at 3' side: hypothetical protein LOC158219

Score = 41.0 bits (44), Expect = 2.0  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query 152      AAGAAAAACAGACCAACAGAAAAGCAA 178
               |||
Sbjct 14873559 AAGAAAAACAGAACACAGCAAAGCAA 14873585
```

>ref|NW\_001839149.2|Hs9\_WGA542\_36 Homo sapiens chromosome 9 genomic contig, alternat  
(based on HuRef SCAF\_1103279188402)  
Length=35741120

Features flanking this part of subject sequence:

288290 bp at 5' side: hypothetical protein LOC158219  
14596 bp at 3' side: FRAS1 related extracellular matrix 1

Score = 41.0 bits (44), Expect = 2.0  
Identities = 25/27 (92%), Gaps = 0/27 (0%)  
Strand=Plus/Minus

```
Query 152      AAGAAAAACAGACCAACAGAAAAGCAA 178
               |||
Sbjct 21021360 AAGAAAAACAGAACACAGCAAAGCAA 21021334
```

>ref|NW\_001837932.2|Hs10\_WGA641\_36 Homo sapiens chromosome 10 genomic contig, altern  
(based on HuRef SCAF\_1103279188217B)  
Length=7623348

Features flanking this part of subject sequence:

11466 bp at 5' side: connexin40.1  
24935 bp at 3' side: cyclin Y isoform 1

Score = 41.0 bits (44), Expect = 2.0  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Minus

```
Query 154      GAAAAACAGACCAACAGAAAAGCAA 178
               |||
Sbjct 2804781  GAAAAACAGAACACAGAAAAGCAA 2804757
```

>ref|NW\_001838052.1|Hs12\_WGA761\_36 Homo sapiens chromosome 12 genomic contig, altern  
(based on HuRef SCAF\_1103279188408)  
Length=21675488

Features flanking this part of subject sequence:

149615 bp at 5' side: intermediate filament tail domain containing 1  
351841 bp at 3' side: Ras association (RalGDS/AF-6) domain family 8

Score = 41.0 bits (44), Expect = 2.0  
Identities = 24/25 (96%), Gaps = 0/25 (0%)  
Strand=Plus/Plus

```
Query 140      TAAAAGCAGCCCAAGAAAAACAGAC 164
```

```

                |||
Sbjct  16266157  TAAAGCAGCCCAAGAAAAACAGAC  16266181

```

```

>ref|NW_001838028.2|Hs11_WGA737_36 Homo sapiens chromosome 11 genomic contig, altern
(based on HuRef SCAF_1103279187758)
Length=16912879

```

```

Features in this part of subject sequence:
  transmembrane protein 135

```

```

Score = 41.0 bits (44), Expect = 2.0
Identities = 27/29 (93%), Gaps = 1/29 (3%)
Strand=Plus/Plus

```

```

Query  141      AAAAGCAGCCCAAGAAAAACAGACCAACA  169
                |||
Sbjct  826512    AAAAGCAGCCCAAGAAAAA-AGACCCACA  826539

```

```

>ref|XM_001715194.1| PREDICTED: Homo sapiens WD repeat domain 42C (WDR42C), mRNA
Length=2979

```

```

Score = 39.2 bits (42), Expect = 6.8
Identities = 30/36 (83%), Gaps = 0/36 (0%)
Strand=Plus/Minus

```

```

Query  157      AACAGACCAACAGAAAAGCAATGAGAGAAAGGATG  192
                ||| | |||| | | |||| ||||| |||
Sbjct  2587      AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAATG  2552

```

```

>ref|XM_293354.9| PREDICTED: Homo sapiens WD repeat domain 42C (WDR42C), mRNA
Length=2983

```

```

Score = 39.2 bits (42), Expect = 6.8
Identities = 30/36 (83%), Gaps = 0/36 (0%)
Strand=Plus/Minus

```

```

Query  157      AACAGACCAACAGAAAAGCAATGAGAGAAAGGATG  192
                ||| | |||| | | |||| ||||| |||
Sbjct  2587      AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAATG  2552

```

```

>ref|XM_942624.3| PREDICTED: Homo sapiens WD repeat domain 42C (WDR42C), mRNA
Length=2684

```

```

Score = 39.2 bits (42), Expect = 6.8
Identities = 30/36 (83%), Gaps = 0/36 (0%)
Strand=Plus/Minus

```

```

Query  157      AACAGACCAACAGAAAAGCAATGAGAGAAAGGATG  192
                ||| | |||| | | |||| ||||| |||
Sbjct  2587      AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAATG  2552

```

```

>ref|NT_025741.14|Hs6_25897 Homo sapiens chromosome 6 genomic contig, reference asse
Length=61645385

```

```

Features flanking this part of subject sequence:

```

65086 bp at 5' side: golgi associated PDZ and coiled-coil motif containing iso...  
8267 bp at 3' side: nuclear undecaprenyl pyrophosphate synthase 1 homolog

Score = 39.2 bits (42), Expect = 6.8  
Identities = 27/31 (87%), Gaps = 0/31 (0%)  
Strand=Plus/Plus

```
Query    166      AACAGAAAAGCAATGAGAGAAAGGATGAAGG      196
          |||||
Spict    22157966 AACAGAAAAGCAAAGACAGAAAAAGATTAAAGG      22157996
```

>ref|NT\_022517.17|Hs3\_22673 Homo sapiens chromosome 3 genomic contig, reference assemblage  
Length=66080833

Features flanking this part of subject sequence:

6402 bp at 5' side: SREBF chaperone protein  
46654 bp at 3' side: transmembrane protein 103

Score = 39.2 bits (42), Expect = 6.8  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```

Query 170          GAAAAGCAATGAGAGAAAGGA 190
                   |||||
Sbjct 47430889     GAAAAGCAATGAGAGAAAGGA 47430909

```

```
>ref|NT_026437.11|Hs14_26604 Homo sapiens chromosome 14 genomic contig, reference as
Length=88290585
```

Features in this part of subject sequence:

pellino 2

Score = 39.2 bits (42), Expect = 6.8  
Identities = 24/27 (88%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query 266      GATCCAGCACAANAAGGNGGNAAGGG 292
                |||||
Sbjct 37708443 GATCCAGCACAAGAAGCGGCAAGGG 37708469
```

```
>ref|NT_006576.15|Hs5_6733 Homo sapiens chromosome 5 genomic contig, reference assem
Length=46378398
```

Features flanking this part of subject sequence:

1398867 bp at 5' side: cadherin 12, type 2 preproprotein  
31459 bp at 3' side: PR domain containing 9

Score = 39.2 bits (42), Expect = 6.8  
Identities = 31/35 (88%), Gaps = 2/35 (5%)  
Strand=Plus/Plus

Query	152	AAGAAAAACAGACCAACAGAAAAGCAATGAGAGAA	186
Spict	23450409	AAGAAAAATAGACCAACAGAACAG-AAT-AGAGAA	23450441

```
>ref|NT_016354.18|Hs4_16510 Homo sapiens chromosome 4 genomic contig, reference asse
```

Length=92123751

Features flanking this part of subject sequence:  
1597372 bp at 5' side: FAT tumor suppressor homolog 4  
532822 bp at 3' side: hypothetical protein

Score = 39.2 bits (42), Expect = 6.8  
Identities = 24/26 (92%), Gaps = 0/26 (0%)  
Strand=Plus/Plus

```

Query 152      AAGAAAAACAGACCAACAGAAAAGCA 177
                |||||
Sbjct 52558442 AAGAAAAACAAACCAACAGAAAATCA 52558467

```

>ref|NT\_011757.15|HsX\_11914 Homo sapiens chromosome X genomic contig, reference assemblage  
Length=34879939

Features flanking this part of subject sequence:  
182 bp at 5' side: similar to hCG19378  
72299 bp at 3' side: melanoma antigen family B, 10

Score = 39.2 bits (42), Expect = 6.8  
Identities = 30/36 (83%), Gaps = 0/36 (0%)  
Strand=Plus/Minus

```

Query 157      AAACAGACCAACAGAAAAGCAATGAGAGAAAGGATG 192
                ||| | |||| | | ||| ||||| |||
Sbjct 25548808 AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAAATG 25548773

```

```
>ref/NT_022135.15|Hs2_22291 Homo sapiens chromosome 2 genomic contig, reference asse
Length=38390280
```

Features in this part of subject sequence:  
contactin associated protein-like 5

Score = 39.2 bits (42), Expect = 6.8  
Identities = 36/46 (78%), Gaps = 0/46 (0%)  
Strand=Plus/Plus

```

Query 151      CAAGAAAAACAGACCAACAGAAAAGCAATGAGAGAAAGGATGAAGG 196
               ||| ||||| ||||| ||||| ||| | | ||| |||||
Sbjct 13818771 CAACAAAAACAGACCAAAAAAAAAAAAAAAAAAAGATGAAGG 13818816

```

```
>ref/NT_005334.15|Hs2_5491 Homo sapiens chromosome 2 genomic contig, reference assem
Length=11088087
```

Features flanking this part of subject sequence:  
189392 bp at 5' side: hypothetical protein LOC348738  
19739 bp at 3' side: hippocalcin-like 1

Score = 39.2 bits (42), Expect = 6.8  
Identities = 27/31 (87%), Gaps = 0/31 (0%)  
Strand=Plus/Plus

```

Query 165      CAACAGAAAAGCAATGAGAGAAAGGATGAAG 195
               |||||  ||  || ||||| ||||| |||
Sbjct 5374250  CAACAAAACAGAAATGAGAGAAAGGATCAAG 5374280

```



>ref|NT\_022184.14|Hs2\_22340 Homo sapiens chromosome 2 genomic contig, reference assemblage  
Length=68373980

Features in this part of subject sequence:  
ATPase family, AAA domain containing 2B

Score = 39.2 bits (42), Expect = 6.8  
Identities = 26/29 (89%), Gaps = 0/29 (0%)  
Strand=Plus/Plus

```
Query 157      AACAGACCAACAGAAAAGCAATGAGAGA 185
                |||
Sbjct 2952937 AACAGACCAACAGAAAAGAACAGAGAGA 2952965
```

>ref|NT\_010194.16|Hs15\_10351 Homo sapiens chromosome 15 genomic contig, reference assemblage  
Length=53619965

Features in this part of subject sequence:  
RAR-related orphan receptor A isoform b  
RAR-related orphan receptor A isoform c

Score = 39.2 bits (42), Expect = 6.8  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Minus

```
Query 158      AACAGACCAACAGAAAAGCAA 178
                |||
Sbjct 31676505 AACAGACCAACAGAAAAGCAA 31676485
```

>ref|NT\_023133.12|Hs5\_23289 Homo sapiens chromosome 5 genomic contig, reference assemblage  
Length=25714846

Features in this part of subject sequence:  
RAN binding protein 17

Score = 39.2 bits (42), Expect = 6.8  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Minus

```
Query 142      AAAGCAGCCCAAGAAAAACAG 162
                |||
Sbjct 15287688 AAAGCAGCCCAAGAAAAACAG 15287668
```

>ref|NW\_001838218.2|Hs15\_WGA927\_36 Homo sapiens chromosome 15 genomic contig, alternate assembly  
(based on HuRef SCAF\_1103279188258)  
Length=30371087

Features in this part of subject sequence:  
RAR-related orphan receptor A isoform c  
RAR-related orphan receptor A isoform b

Score = 39.2 bits (42), Expect = 6.8  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```

Query   158          AACAGACCAACAGAAAAGCAA   178
          |||||
Sbjct   13482804    AACAGACCAACAGAAAAGCAA   13482824

```

>ref|NW\_001838848.1|Hs2\_WGA241\_36 Homo sapiens chromosome 2 genomic contig, alternat  
(based on HuRef SCAF\_1103279188208)  
Length=5768927

Features in this part of subject sequence:  
contactin associated protein-like 5

Score = 39.2 bits (42), Expect = 6.8  
Identities = 36/46 (78%), Gaps = 0/46 (0%)  
Strand=Plus/Plus

```

Query   151          CAAGAAAAACAGACCAACAGAAAAGCAATGAGAGAAAGGATGAAGG   196
          ||| |||||
Sbjct   3959290    CAACAAAAACAGACCAAAAAAAGATGAAGG   3959335

```

>ref|NW\_001838768.1|Hs2\_WGA161\_36 Homo sapiens chromosome 2 genomic contig, alternat  
(based on HuRef SCAF\_1103279188306)  
Length=8993619

Features in this part of subject sequence:  
ATPase family, AAA domain containing 2B

Score = 39.2 bits (42), Expect = 6.8  
Identities = 26/29 (89%), Gaps = 0/29 (0%)  
Strand=Plus/Plus

```

Query   157          AAACAGACCAACAGAAAAGCAATGAGAGA   185
          |||||
Sbjct   2966183    AAACAGACCAACAGAAAAGAACAGAGAGA   2966211

```

>ref|NW\_001838766.1|Hs2\_WGA159\_36 Homo sapiens chromosome 2 genomic contig, alternat  
(based on HuRef SCAF\_1103279187422)  
Length=8347242

Features flanking this part of subject sequence:  
190464 bp at 5' side: hypothetical protein LOC348738  
19733 bp at 3' side: hippocalcin-like 1

Score = 39.2 bits (42), Expect = 6.8  
Identities = 27/31 (87%), Gaps = 0/31 (0%)  
Strand=Plus/Plus

```

Query   165          CAACAGAAAAGCAATGAGAGAAAGGATGAAG   195
          ||||| || || |||||
Sbjct   2637447    CAACAAAACAGAAATGAGAGAAAGGATCAAG   2637477

```

>ref|NW\_001838920.1|Hs4\_WGA313\_36 Homo sapiens chromosome 4 genomic contig, alternat  
(based on HuRef SCAF\_1103279188303)  
Length=20364230

Features flanking this part of subject sequence:  
1597064 bp at 5' side: FAT tumor suppressor homolog 4

532542 bp at 3' side: hypothetical protein

Score = 39.2 bits (42), Expect = 6.8  
Identities = 24/26 (92%), Gaps = 0/26 (0%)  
Strand=Plus/Plus

```
Query 152      AAGAAAAACAGACCAACAGAAAAGCA 177
               ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 8584868  AAGAAAAACAAACCAACAGAAAATCA 8584893
```

>ref|NW\_001838929.1|Hs5\_WGA322\_36 Homo sapiens chromosome 5 genomic contig, alternat  
(based on HuRef SCAF\_1103279188406C)  
Length=12799137

Features flanking this part of subject sequence:  
1399583 bp at 5' side: cadherin 12, type 2 preproprotein  
31453 bp at 3' side: PR domain containing 9

Score = 39.2 bits (42), Expect = 6.8  
Identities = 31/35 (88%), Gaps = 2/35 (5%)  
Strand=Plus/Plus

```
Query 152      AAGAAAAACAGACCAACAGAAAAGCAATGAGAGAA 186
               ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 2083999  AAGAAAAATAGACCAACAGAACAG- AAT-AGAGAA 2084031
```

>ref|NW\_001838111.1|Hs14\_WGA820\_36 Homo sapiens chromosome 14 genomic contig, altern  
(based on HuRef SCAF\_1103279187954)  
Length=25156336

Features in this part of subject sequence:  
pellino 2

Score = 39.2 bits (42), Expect = 6.8  
Identities = 24/27 (88%), Gaps = 0/27 (0%)  
Strand=Plus/Plus

```
Query 266      GATCCAGCACAAAGGNGGNAAGGG 292
               ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 15574420  GATCCAGCACAAAGGCGGCAAGGG 15574446
```

>ref|NW\_001842360.1|HsX\_WGA1321\_36 Homo sapiens chromosome X genomic contig, alterna  
(based on HuRef SCAF\_1103279188416)  
Length=28681338

Features flanking this part of subject sequence:  
182 bp at 5' side: hypothetical protein  
72349 bp at 3' side: melanoma antigen family B, 10

Score = 39.2 bits (42), Expect = 6.8  
Identities = 30/36 (83%), Gaps = 0/36 (0%)  
Strand=Plus/Minus

```
Query 157      AAACAGACCAACAGAAAAGCAATGAGAGAAAGGATG 192
               ||| | ||| || ||| ||| ||| ||| |||
Sbjct 19297887  AAAGAAACCAAGAGGAAAGGAATGAGAGAAAGAAATG 19297852
```

>ref|NW\_001838954.2|Hs5\_WGA347\_36 Homo sapiens chromosome 5 genomic contig, alternat  
(based on HuRef SCAF\_1103279188298)  
Length=20179980

Features in this part of subject sequence:  
RAN binding protein 17

Score = 39.2 bits (42), Expect = 6.8  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Plus

```
Query 142      AAAGCAGCCCCAAGAAAAACAG 162
               |||
Sbjct 4886351 AAAGCAGCCCCAAGAAAAACAG 4886371
```

>ref|NW\_001838877.2|Hs3\_WGA270\_36 Homo sapiens chromosome 3 genomic contig, alternat  
(based on HuRef SCAF\_1103279188143)  
Length=55925128

Features flanking this part of subject sequence:  
46504 bp at 5' side: transmembrane protein 103  
6392 bp at 3' side: SREBF chaperone protein

Score = 39.2 bits (42), Expect = 6.8  
Identities = 21/21 (100%), Gaps = 0/21 (0%)  
Strand=Plus/Minus

```
Query 170      GAAAAGCAATGAGAGAAAGGA 190
               |||
Sbjct 18731141 GAAAAGCAATGAGAGAAAGGA 18731121
```

Database: Human build 36.3 RNA, reference, and HuRef assemblies  
Posted date: Dec 2, 2008 11:49 AM  
Number of letters in database: 1,523,044,440  
Number of sequences in database: 49,942

```
Lambda      K      H
0.634      0.408    0.912
```

Gapped

```
Lambda      K      H
0.625      0.410    0.780
```

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 49942

Number of Hits to DB: 1626165

Number of extensions: 83827

Number of successful extensions: 160

Number of sequences better than 10: 4

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 160

Number of HSP's successfully gapped: 4

Length of query: 754

Length of database: 5818011736

Length adjustment: 34

Effective length of query: 720

Effective length of database: 5816313708

Effective search space: 4187745869760  
Effective search space used: 4187745869760  
A: 0  
X1: 22 (20.1 bits)  
X2: 33 (29.8 bits)  
X3: 110 (99.2 bits)  
S1: 34 (31.9 bits)  
S2: 42 (39.2 bits)